Identification of mutations in the para sodium channel gene (*kdr*) and in Acetylcholinesterase gene (*Ace-1^R*) of *Bemisia tabaci* (Hemiptera: Aleyrodidae) from Western Africa

First International Whitefly Symposium
20-24 May 2013, Kolymbari, Crete, Greece

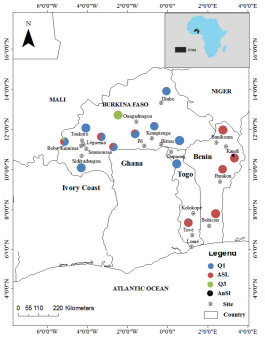
O. Gnankiné[1], L. Mouton[2],T. Martin[3], G. Ketoh[4], F. Vavre[2] & F. Fleury[2]

1 Laboratoire d'Entomologie Fondamentale et Appliquée, Université de Ouagadougou, Burkina Faso, 2 Laboratoire de Biométrie et Biologie Evolutive, UMR 5558, Université de Lyon, CNRS, Villeurbanne, France; 3 UR Hortsys, Cirad, Montpellier, France; 4 Université de Lomé, Togo

INTRODUCTION

The world pest *Bemisia tabaci* (Gennadius) is a complex of morphologically indistinguishable species that differ with regard to various biological characteristics, notably insecticide resistance. The Mediterranean **(MED)** species include genetic groups known as biotypes **Q, J, L** and sub-Saharan Africa Silverleaf **(ASL)** and shows multiple resistances to Organophosphate (OP) and Pyrethroids (Py). These genetic groups sometime coexist in the same area such as in Africa where admixture, hybridization and recombination may occur. However, no or very few data are available about occurrence and frequency of resistance alleles in natural mixed populations. This study aim to measure the frequency of ***kdr*** and ***ace-1^R*** mutations within and among *B. tabaci* genetic groups in three countries of western Africa (Burkina Faso, Benin and Togo).

Figure 1: Sampling areas and distribution of *B. tabaci* MED species genetic groups in West Africa



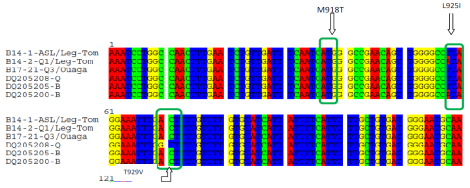
MATERIALS AND METHODS

- Identification of the biotypes in West Africa by **PCR/RFLP** of 454 individuals collected from 19 localities and 6 cultivated host plants
- Seek of ***F331W*** mutation in the acetylcholinesterase enzyme ace1 and **(L925I)** or **(T929V)** mutation in the para-type voltage gated sodium channel (*kdr*) by PCR followed of sequencing of 43 samples (18 samples of Q1, 15 of ASL and 10 of Q3), according to the host plant and the geographical position.

Table 1 : Frequencies of sodium channel and ace-1 resistant mutations in *B. tabaci* (only males) by PCR/RFLP

				Alleles frequencies			
				Ace1		L925I	
Country	Locality	Host plant	Biotype	R	S	R	S
Burkina Faso	U. Ouaga	*L. Camara*	Q3	0	1	0	1
Burkina Faso	Léguema	Tomato	Q1	1	0	1	0
Burkina Faso	Léguema	Tomato	ASL	1	0	0	1
Burkina Faso	Bobo/koko	Cotton	Q1	0.66	0.34	1	0
Benin	Parakou	Cotton	ASL	1	0	0	1
Togo	Infa	Cotton	ASL	1	0	0	1

Figure 3: Clustal alignment indicates mutations found in the transmembrane segment IIS4 of the para sodium channel gene



RESULTS

- **Important diversity** of biotypes in the 3 countries of western Africa (Burkina Faso, Benin and Togo) (Fig. 1 & 2).
- ✓ **Q1** was predominant in Burkina Faso.
- ✓ **ASL** biotype show high frequencies in Benin and Togo.
- ***Ace1* gene** (F331W) linked to OP resistance, was observed in Q1 and ASL individuals, but not in Q3 individuals (*table1, Fig. 3 & 4*).
- ***kdr* gene** (L925I) linked to pyrethroid resistance, was observed only in Q1 individuals (*table1, Fig. 3 & 4*).
- These results clearly indicate that different genetic groups co-exist in West Africa and exhibit variations for insecticide resistance.

Figure 2: Representative gels showing ASL and Q1 biotypescollected in Burkina Faso. Lanes 1, 2, 3, 4: Q1 biotype; Lanes 5,6,7 8: ASL biotype, digested with XapI. M: Hyper ladder IV

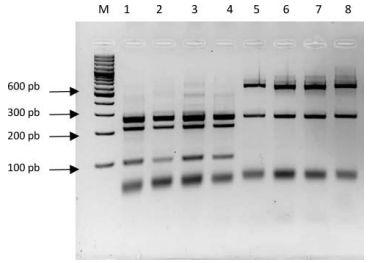
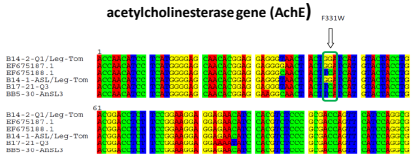


Figure 4: Clustal alignment indicates mutations found in the in the acetylcholinesterase gene (AchE)



CONCLUSION

- Pest management program should take into account:
  - **Diversity** within species and genetic groups (biotypes)
  - Resistance to OP and pyrethroid encountered in these countries
    - ✓**efficiency of insecticide** treatments will greatly vary according to the genetic groups present,
    - ✓ treatments may favor invasion of **Q1**, one of the most dangerous biotype of *B. tabaci* and already resistant to **neonicotinoid**.